

# Transcriptomic changes in boron tolerant *Triticum zhukovskyi* genotype under high boron

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## NEED & AIM OF THE STUDY

- Boron toxicity hinders the wheat production around the world in arid and semi-arid regions (Pallotta et al. 2014).
- New wheat genetic resources with higher boron toxicity tolerance are required to reduce this wheat loss.
- Triticum zhukovskyi* is a hexaploid cultivated neglected wheat species with AAAAGG genome.**
- It is previously explored for resistance towards various biotic stresses such as stem rust, fusarium head blight, leaf rust etc. but limited reports are available on their abiotic stress tolerance.
- No previous reports on its boron toxicity tolerance and the involved tolerance mechanism.**
- Aim was to determine the transcriptomic changes occurring in the boron tolerant, *T. zhukovskyi* genotype (PI296968) (Figure 1) under boron toxic growth conditions as compared to Control.**

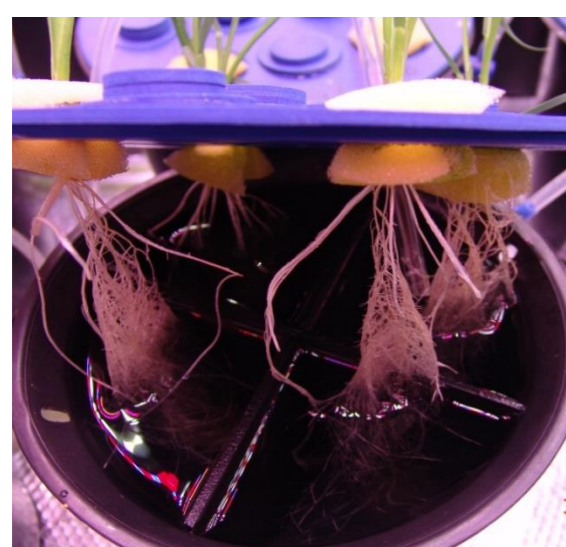


**Figure 1.** For the first time, any *T. zhukovskyi* genotype (PI296968) was reported to be more tolerant than the well-recognized boron tolerant hexaploid wheat cultivar, Bolal 2973 under toxic boron supply (10 mM boron)

NOVELTY

## METHOD

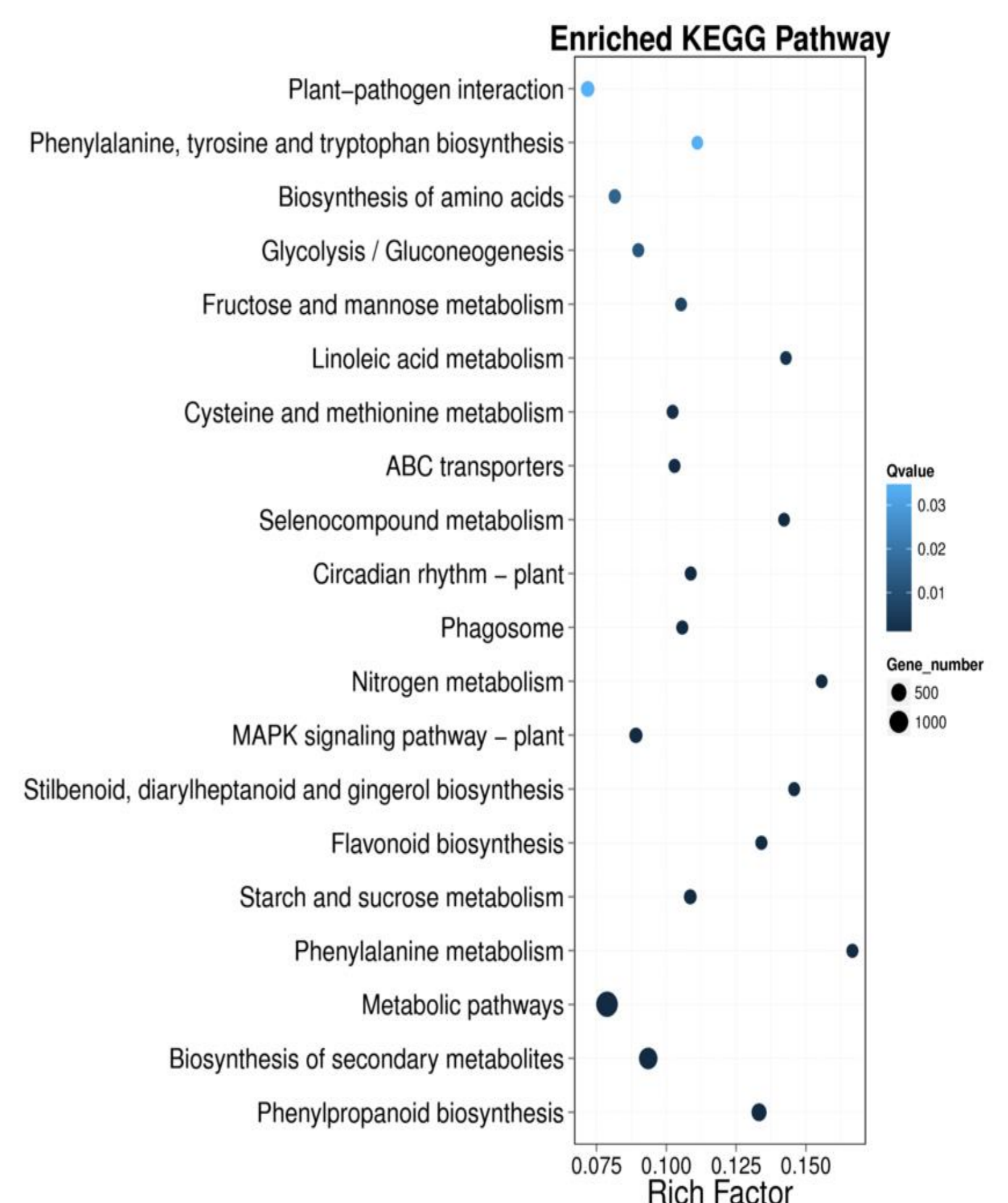
- The *T. zhukovskyi* genotype was grown in Control (3.1  $\mu$ M) and Highly Toxic Boron (10 mM) in hydroponic growth conditions for 7 days (Figure 2)
- RNA sequencing of root RNA samples from both treatments was conducted.
- Significant Differentially Expressed Genes (DEGs) under boron toxicity were determined and their Functional Annotation and Pathway Enrichment Analysis was performed. DEGs encoding Transcription Factors were also identified.



**Figure 2.** Roots of the *T. zhukovskyi* genotype grown in high boron for one week

## MAIN RESULTS

- A total of **5992 genes showed significant differential expression** under high boron.
- Potential candidate genes were involved in biological regulation, metabolic processes, cellular processes, responses to stimulus, membranes, cells, catalytic activity, and binding activity.
- Transcription factors of ***MYB* and *MYB-related*, *WRKY*, *NAC*, *bZIP*, and *bHLH* families** were significantly enriched under boron toxicity.
- Maximum enrichment of DEGs was observed in phenylalanine metabolism and nitrogen metabolism pathways** (Figure 3).



**Figure 3.** Enriched KEGG Pathways

## CONCLUSION

- A number of genes participating in different crucial pathways can be possibly involved in providing boron toxicity tolerance to the *T. zhukovskyi* genotype.
- Identified boron toxicity stress responsive candidate genes could facilitate additional omics studies in wheat and other cereal crops.
- Potential candidate genes can be used to enlarge the limited genetic diversity of modern wheat cultivars via molecular breeding or genetic engineering.

## FUTURE RESEARCH

Further research including transgenic experiments and subcellular characterization is required to functionally characterize the identified high-boron responsive genes to confirm their role in providing boron toxicity tolerance.

## REFERENCES

- Pallotta et al. (2014) Molecular basis of adaptation to high soil boron in wheat landraces and elite cultivars. *Nature* 514 (7520) : 88-91.
- Pandey et al. (2022) Insight into the root transcriptome of a boron-tolerant *Triticum zhukovskyi* genotype grown under boron toxicity. *Agronomy*, 12(10), 2421.